



P1066P2.txt

Sequence Listing

<110> Lasky, Laurence A.  
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated  
Proteins (PSTPIPs)

<130> P1066P2

<140> US 09/068,377

<141> 1998-05-08

<150> PCT/US98/01774

<151> 1998-01-30

<150> US 08/938,830

<151> 1997-09-29

<150> US 08/798,419

<151> 1997-02-07

<160> 76

<210> 1

<211> 415

<212> PRT

<213> Mus Musculus

<400> 1

Met Met Ala Gln Leu Gln Phe Arg Asp Ala Phe Trp Cys Arg Asp  
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Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu  
20 25 30

Asp Gly Arg Lys Met Cys Lys Asp Val Glu Glu Leu Leu Arg Gln  
35 40 45

Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile  
50 55 60

Ala Arg Lys Ala Gly Gly Gln Thr Glu Met Asn Ser Leu Arg Thr  
65 70 75

Ser Phe Asp Ser Leu Lys Gln Gln Thr Glu Asn Val Gly Ser Ala  
80 85 90

His Ile Gln Leu Ala Leu Ala Leu Arg Glu Glu Leu Arg Ser Leu  
95 100 105

Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Tyr Glu  
110 115 120

Ala Ile Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys  
125 130 135

Lys Thr Met Glu Ser Lys Lys Ala Tyr Asp Gln Lys Cys Arg Asp  
140 145 150



P1066P2.txt

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asp | Asp | Ala | Glu | Gln | Ala | Phe | Glu | Arg | Val | Ser | Ala | Asn | Gly |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |
| His | Gln | Lys | Gln | Val | Glu | Lys | Ser | Gln | Asn | Lys | Ala | Lys | Gln | Cys |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |
| Lys | Glu | Ser | Ala | Thr | Glu | Ala | Glu | Arg | Val | Tyr | Arg | Gln | Asn | Ile |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |
| Glu | Gln | Leu | Glu | Arg | Ala | Arg | Thr | Glu | Trp | Glu | Gln | Glu | His | Arg |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
| Thr | Thr | Cys | Glu | Ala | Phe | Gln | Leu | Gln | Glu | Phe | Asp | Arg | Leu | Thr |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Ile | Leu | Arg | Asn | Ala | Leu | Trp | Val | His | Cys | Asn | Gln | Leu | Ser | Met |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Cys | Val | Lys | Asp | Asp | Glu | Leu | Tyr | Glu | Glu | Val | Arg | Leu | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Leu | Glu | Gly | Cys | Asp | Val | Glu | Gly | Asp | Ile | Asn | Gly | Phe | Ile | Gln |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |
| Ser | Lys | Ser | Thr | Gly | Arg | Glu | Pro | Pro | Ala | Pro | Val | Pro | Tyr | Gln |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |
| Asn | Tyr | Tyr | Asp | Arg | Glu | Val | Thr | Pro | Leu | Ile | Gly | Ser | Pro | Ser |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |
| Ile | Gln | Pro | Ser | Cys | Gly | Val | Ile | Lys | Arg | Phe | Ser | Gly | Leu | Leu |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |
| His | Gly | Ser | Pro | Lys | Thr | Thr | Pro | Ser | Ala | Pro | Ala | Ala | Ser | Thr |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |
| Glu | Thr | Leu | Thr | Pro | Thr | Pro | Glu | Arg | Asn | Glu | Leu | Val | Tyr | Ala |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |
| Ser | Ile | Glu | Val | Gln | Ala | Thr | Gln | Gly | Asn | Leu | Asn | Ser | Ser | Ala |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |
| Gln | Asp | Tyr | Arg | Ala | Leu | Tyr | Asp | Tyr | Thr | Ala | Gln | Asn | Ser | Asp |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |
| Glu | Leu | Asp | Ile | Ser | Ala | Gly | Asp | Ile | Leu | Ala | Val | Ile | Leu | Glu |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |
| Gly | Glu | Asp | Gly | Trp | Trp | Thr | Val | Glu | Arg | Asn | Gly | Gln | Arg | Gly |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |
| Phe | Val | Pro | Gly | Ser | Tyr | Leu | Glu | Lys | Leu |     |     |     |     |     |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     |     |

<210> 2

<211> 2100

<212> DNA

<213> Mus Musculus

<400> 2

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agaagaagcg gaaggtctcg agcggcgcca attttaatca aagtgggaat 100



P1066P2.txt

attgctgata gctcattgtc cttcactttc actaacagta gcaacgggtcc 150  
 gaacctcata acaactcaaa caaattctca agcgctttca caaccaattg 200  
 cctcctctaa cgttcatgat aacttcatga ataataaaat cacggctagt 250  
 aaaattgatg atggtaataa ttcaaaaacca ctgtcacctg gttggacgga 300  
 ccaaactgcy tataacgcgt ttggaatcac tacagggatg tttaatacca 350  
 ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccca 400  
 ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gctccttcct 450  
 catttcgctg ctgattctag ccccaaaca aacagggtga gcctttttcc 500  
 tcctccggca gttgcctctg gcttgtggct gccttctgag cgtttcagac 550  
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 gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650  
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 tccgagatgc cttctggtgc agggacttca cggccacac agggatatgag 750  
 gtgctactgc agaggctgct ggacggcagg aagatgtgca aggatgtgga 800  
 ggagctgctc agacagaggg cccaggcgga ggagaggtag gggaaggagc 850  
 tgggtcagat tgcacgcaag gctggtggcc agacagagat gaattccctg 900  
 aggacctcct ttgactccct gaagcagcaa acagagaatg tgggcagtgc 950  
 acacatccag ctggccctgg ccctgcgtga ggagctgcgg agcctggagg 1000  
 agttccgaga gagacagaaa gagcagcgga agaagtatga ggccatcatg 1050  
 gaccgtgtcc agaagagcaa gttgtcgctc tacaagaaga ccatggagtc 1100  
 caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150  
 ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200  
 cagaacaaag ccaagcagt caaggagtca gccacagagg cagaaagagt 1250  
 gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300  
 aggagcaccg gactacctgt gaggccttcc agttgcagga gtttgaccgg 1350  
 ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400  
 gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450  
 agggctgtga tgtggaaggt gacatcaatg gtttcatcca gtccaagagc 1500  
 actggcagag agccccagc tccggtgcct tatcagaact actatgacag 1550  
 ggaggtgacc ccactgattg gcagccctag catccagccc tcctgcggtg 1600  
 tgataaagag gttctctggg ctgctacatg gaagtcctaa gaccacacct 1650



P1066P2.txt

tctgctcctg ctgcttccac agagactctg actcccaccc ctgagcggaa 1700  
 tgagttggtc tacgcatcca tcgaagtgca ggcgaccag ggaaacctta 1750  
 actcatcagc ccaggactac cgggcactct acgactacac tgcacagaat 1800  
 tctgatgagc tggacatttc cgcgggagac atcctggcgg tcatcctgga 1850  
 aggggaggat ggctgggtgga ctgtggagcg gaacggacaa cgtggctttg 1900  
 tccctgggtc gtacttggag aagctctgag gaaaggctag cagtctccac 1950  
 atacctccgc cctgactgtg aggtcaggac tgtttctttc catcaccgcc 2000  
 caggcctcac ggggccagaa ccaagcccgg tggtgctggg catgggctgg 2050  
 gtgctggcta ctctcaataa atgtctccca gaaggaaaaa aaaaaaaaaa 2100

<210> 3  
 <211> 48  
 <212> PRT  
 <213> Mus Musculus

<400> 3  
 Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser  
 1 5 10 15  
 Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp  
 20 25 30  
 Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser  
 35 40 45  
 Tyr Leu Arg

<210> 4  
 <211> 50  
 <212> PRT  
 <213> Homo sapien

<400> 4  
 Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn  
 1 5 10 15  
 Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp  
 20 25 30  
 Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn  
 35 40 45  
 Tyr Val Glu Lys Ile  
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<210> 5  
 <211> 50  
 <212> PRT  
 <213> Homo sapien

<400> 5  
 Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys  
 1 5 10 15



P1066P2.txt

Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp  
20 25 30

Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala  
35 40 45

Tyr Val Lys Lys Leu  
50

<210> 6  
<211> 50  
<212> PRT  
<213> Homo sapien

<400> 6  
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1 5 10 15

Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp  
20 25 30

Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn  
35 40 45

Tyr Val Lys Leu Leu  
50

<210> 7  
<211> 48  
<212> PRT  
<213> Homo sapien

<400> 7  
Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp  
1 5 10 15

Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp  
20 25 30

Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn  
35 40 45

Tyr Val Glu

<210> 8  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Amino acid epitope tag

<400> 8  
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1 5

<210> 9  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Synthetic oligonucleotide probe

<400> 9  
cgcggatcca ccatgatggc ccagctgcag ttc 33

<210> 10

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 11

<211> 18

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 11  
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<210> 12

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 12  
ctccttgagg ttctactagt gggggctggt gtcctg 36

<210> 13

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 14

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14  
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<210> 15

<211> 41

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

ttatagtttta gcggccgctc accggtagtc ctgggctgat g 41

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16

gtacgcgtcg accgcactct acgactacac tgcacag 37

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

ctctggcgaa gaagtcc 17

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

gacgaattc ccagaacctc aaggagaact gc 32

<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 19

gacctcgcg ttacacccgt gtccactctg ctggagga 38

<210> 20

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic oligopeptide

<400> 20

Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro

1

5

10

15



Pro Ala Glu Trp Thr  
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<210> 21  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic oligopeptide

<400> 21  
Gly Phe Gly Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro  
1 5 10 15

Pro Ser Ala Trp

<210> 22  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic oligopeptide

<400> 22  
Gly Phe Gly Asn Arg Cys Gly Lys Pro Lys Gly Pro Arg Asp Pro  
1 5 10 15

Pro Ser Glu Trp Thr  
20

<210> 23  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic oligopeptide

<400> 23  
Gly Gly Val Leu Arg Ser Ile Ser Val Pro Ala Pro Pro Thr Leu  
1 5 10 15

Pro Met Ala Asp Thr  
20

<210> 24  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
gtatatgtcc tggccagccc atgggggttcc cagcag 36

<210> 25  
<211> 36  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

gcaggctcgac tctagattac acccgtgtcc actctg 36

<210> 26

<211> 907

<212> PRT

<213> Saccharomyces Pombe

<400> 26

Met Leu Thr Lys Ser Leu Gln Gly Ser Glu Asp Ala Gly Met Asp  
1 5 10 15

Ala Leu Met Ser Arg Thr Lys Ser Ser Leu Ser Val Leu Glu Ser  
20 25 30

Ile Asp Glu Phe Tyr Ala Lys Arg Ala Ser Ile Glu Arg Glu Tyr  
35 40 45

Ala Ser Lys Leu Gln Glu Leu Ala Ala Ser Ser Ala Asp Ile Pro  
50 55 60

Glu Val Gly Ser Thr Leu Asn Asn Ile Leu Ser Met Arg Thr Glu  
65 70 75

Thr Gly Ser Met Ala Lys Ala His Glu Glu Val Ser Gln Gln Ile  
80 85 90

Asn Thr Glu Leu Arg Asn Lys Ile Arg Glu Tyr Ile Asp Gln Thr  
95 100 105

Glu Gln Gln Lys Val Val Ala Ala Asn Ala Ile Glu Glu Leu Tyr  
110 115 120

Gln Lys Lys Thr Ala Leu Glu Ile Asp Leu Ser Glu Lys Lys Asp  
125 130 135

Ala Tyr Glu Tyr Ser Cys Asn Lys Leu Asn Ser Tyr Met Arg Gln  
140 145 150

Thr Lys Lys Met Thr Gly Arg Glu Leu Asp Lys Tyr Asn Leu Lys  
155 160 165

Ile Arg Gln Ala Ala Leu Ala Val Lys Lys Met Asp Ala Glu Tyr  
170 175 180

Arg Glu Thr Asn Glu Leu Leu Leu Thr Val Thr Arg Glu Trp Ile  
185 190 195

Asp Arg Trp Thr Glu Val Cys Asp Ala Phe Gln His Ile Glu Glu  
200 205 210

Tyr Arg Leu Glu Phe Leu Lys Thr Asn Met Trp Ala Tyr Ala Asn  
215 220 225

Ile Ile Ser Thr Ala Cys Val Lys Asp Asp Glu Ser Cys Glu Lys  
230 235 240

Ile Arg Leu Thr Leu Glu Asn Thr Asn Ile Asp Glu Asp Ile Thr



| 245                                 | 250                     | 255 |
|-------------------------------------|-------------------------|-----|
| Gln Met Ile Gln Asn Glu Gly Thr Gly | Thr Thr Ile Pro Pro     | Leu |
| 260                                 | 265                     | 270 |
| Pro Glu Phe Asn Asp Tyr Phe Lys Glu | Asn Gly Leu Asn Tyr Asp |     |
| 275                                 | 280                     | 285 |
| Ile Asp Gln Leu Ile Ser Lys Ala Pro | Ser Tyr Pro Tyr Ser     | Ser |
| 290                                 | 295                     | 300 |
| Ser Arg Pro Ser Ala Ser Ala Ser Leu | Ala Ser Ser Pro Thr     | Arg |
| 305                                 | 310                     | 315 |
| Ser Ala Phe Arg Pro Lys Thr Ser Glu | Thr Val Ser Ser Glu     | Val |
| 320                                 | 325                     | 330 |
| Val Ser Ser Pro Pro Thr Ser Pro Leu | His Ser Pro Val Lys     | Pro |
| 335                                 | 340                     | 345 |
| Val Ser Asn Glu Gln Val Glu Gln Val | Thr Glu Val Glu Leu     | Ser |
| 350                                 | 355                     | 360 |
| Ile Pro Val Pro Ser Ile Gln Glu Ala | Glu Ser Gln Lys Pro     | Val |
| 365                                 | 370                     | 375 |
| Leu Thr Gly Ser Ser Met Arg Arg Pro | Ser Val Thr Ser Pro     | Thr |
| 380                                 | 385                     | 390 |
| Phe Glu Val Ala Ala Arg Pro Leu Thr | Ser Met Asp Val Arg     | Ser |
| 395                                 | 400                     | 405 |
| Ser His Asn Ala Glu Thr Glu Val Gln | Ala Ile Pro Ala Ala     | Thr |
| 410                                 | 415                     | 420 |
| Asp Ile Ser Pro Glu Val Lys Glu Gly | Lys Asn Ser Glu Asn     | Ala |
| 425                                 | 430                     | 435 |
| Ile Thr Lys Asp Asn Asp Asp Ile Ile | Leu Ser Ser Gln Leu     | Gln |
| 440                                 | 445                     | 450 |
| Pro Thr Ala Thr Gly Ser Arg Ser Ser | Arg Leu Ser Phe Ser     | Arg |
| 455                                 | 460                     | 465 |
| His Gly His Gly Ser Gln Thr Ser Leu | Gly Ser Ile Lys Arg     | Lys |
| 470                                 | 475                     | 480 |
| Ser Ile Met Glu Arg Met Gly Arg Pro | Thr Ser Pro Phe Met     | Gly |
| 485                                 | 490                     | 495 |
| Ser Ser Phe Ser Asn Met Gly Ser Arg | Ser Thr Ser Pro Thr     | Lys |
| 500                                 | 505                     | 510 |
| Glu Gly Phe Ala Ser Asn Gln His Ala | Thr Gly Ala Ser Val     | Gln |
| 515                                 | 520                     | 525 |
| Ser Asp Glu Leu Glu Asp Ile Asp Pro | Arg Ala Asn Val Val     | Leu |
| 530                                 | 535                     | 540 |
| Asn Val Gly Pro Asn Met Leu Ser Val | Gly Glu Ala Pro Val     | Glu |
| 545                                 | 550                     | 555 |
| Ser Thr Ser Lys Glu Glu Asp Lys Asp | Val Pro Asp Pro Ile     | Ala |



| 560                                 | 565                 | 570 |
|-------------------------------------|---------------------|-----|
| Asn Ala Met Ala Glu Leu Ser Ser Ser | Met Arg Arg Arg Gln | Ser |
| 575                                 | 580                 | 585 |
| Thr Ser Val Asp Asp Glu Ala Pro Val | Ser Leu Ser Lys Thr | Ser |
| 590                                 | 595                 | 600 |
| Ser Ser Thr Arg Leu Asn Gly Leu Gly | Tyr His Ser Arg Asn | Thr |
| 605                                 | 610                 | 615 |
| Ser Ile Ala Ser Asp Ile Asp Gly Val | Pro Lys Lys Ser Thr | Leu |
| 620                                 | 625                 | 630 |
| Gly Ala Pro Pro Ala Ala His Thr Ser | Ala Gln Met Gln Arg | Met |
| 635                                 | 640                 | 645 |
| Ser Asn Ser Phe Ala Ser Gln Thr Lys | Gln Val Phe Gly Glu | Gln |
| 650                                 | 655                 | 660 |
| Arg Thr Glu Asn Ser Ala Arg Glu Ser | Leu Arg His Ser Arg | Ser |
| 665                                 | 670                 | 675 |
| Asn Met Ser Arg Ser Pro Ser Pro Met | Leu Ser Arg Arg Ser | Ser |
| 680                                 | 685                 | 690 |
| Thr Leu Arg Pro Ser Phe Glu Arg Ser | Ala Ser Ser Leu Ser | Val |
| 695                                 | 700                 | 705 |
| Arg Gln Ser Asp Val Val Ser Pro Ala | Pro Ser Thr Arg Ala | Arg |
| 710                                 | 715                 | 720 |
| Gly Gln Ser Val Ser Gly Gln Gln Arg | Pro Ser Ser Ser Met | Ser |
| 725                                 | 730                 | 735 |
| Leu Tyr Gly Glu Tyr Asn Lys Ser Gln | Pro Gln Leu Ser Met | Gln |
| 740                                 | 745                 | 750 |
| Arg Ser Val Ser Pro Asn Pro Leu Gly | Pro Asn Arg Arg Ser | Ser |
| 755                                 | 760                 | 765 |
| Ser Val Leu Gln Ser Gln Lys Ser Thr | Ser Ser Asn Thr Ser | Asn |
| 770                                 | 775                 | 780 |
| Arg Asn Asn Gly Gly Tyr Ser Gly Ser | Arg Pro Ser Ser Glu | Met |
| 785                                 | 790                 | 795 |
| Gly His Arg Tyr Gly Ser Met Ser Gly | Arg Ser Met Arg Gln | Val |
| 800                                 | 805                 | 810 |
| Ser Gln Arg Ser Thr Ser Arg Ala Arg | Ser Pro Glu Pro Thr | Asn |
| 815                                 | 820                 | 825 |
| Arg Asn Ser Val Gln Ser Lys Asn Val | Asp Pro Arg Ala Thr | Phe |
| 830                                 | 835                 | 840 |
| Thr Ala Glu Gly Glu Pro Ile Leu Gly | Tyr Val Ile Ala Leu | Tyr |
| 845                                 | 850                 | 855 |
| Asp Tyr Gln Ala Gln Ile Pro Glu Glu | Ile Ser Phe Gln Lys | Gly |
| 860                                 | 865                 | 870 |
| Asp Thr Leu Met Val Leu Arg Thr Gln | Glu Asp Gly Trp Trp | Asp |



875

880

885

Gly Glu Ile Ile Asn Val Pro Asn Ser Lys Arg Gly Leu Phe Pro  
 890 895 900

Ser Asn Phe Val Gln Thr Val  
 905

&lt;210&gt; 27

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Any amino acid

&lt;400&gt; 27

Pro Xaa Xaa Pro

1

&lt;210&gt; 28

&lt;211&gt; 1613

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 28

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 ctatagggct cgagcggccg cccgggcagg tctagaattc agcggccgct 150  
 gaattctctt tttcctcccc tcagaagctc ctctctggct cgtggctgcc 200  
 ttctgagtgt tgcagacggc gccggccggg aagggggggc tgggccagcc 250  
 ctgccaggac tgggacgctg ctgctgacgc ctggccctcc atcaggccag 300  
 cctgtggcag gagagtgagc tttgccgcgg cagacgcctg aggatgatgc 350  
 cccagctgca gttcaaagat gccttttggg gcagggactt cacagcccac 400  
 acgggctacg aggtgctgct gcagcggctt ctggatggca ggaagatgtg 450  
 caaagacatg gaggagctac tgaggcagag ggcccaggcg gaggagcggg 500  
 acgggaagga gctggtgcag atcgacgga aggcagggtg ccagacggag 550  
 atcaactccc tgagggcctc ctttgactcc ttgaagcagc aaatggagaa 600  
 tgtgggcagc tcacacatcc agctggccct gaccctgcgt gaggagctgc 650  
 ggagtctcga ggagtttcgt gagaggcaga aggagcagag gaagaagggc 700  
 atggctgtcc cgagacagag tgactgcatg gaagtgaagt ccccatcatg 750  
 ggagtatgag gccgtcatgg accgggtcca gaagagcaag ctgtcgctct 800  
 acaagaaggc catggagtcc aagaagacat acgagcagaa gtgccggggac 850  
 gcggacgacg cggagcaggc cttcgagcgc attagcgcca acggccacca 900  
 gaagcagggtg gagaagagtc agaacaaagc caggcagtgc aaggactcgg 950



P1066P2.txt

ccaccgaggc agagcgggta tacaggcaga gcattgcgca gctggagaag 1000  
gtccggggtg agtgggagca ggagcaccgg accacctgtg aggcctttca 1050  
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acagtaacca gctctccatg cagtgtgtca aggatgatga gctctacgag 1150  
gaagtgcggc tgacgctgga aggctgcagc atagacgccg acatcgacag 1200  
tttcatccag gccaagagca cgggcacaga gccccccagg ttctctggac 1250  
tgctgcacgg aagtcccaag accacttcgt cagcttctgc tggctccaca 1300  
gagaccctga cccccacccc cgagcgggaat gaggggtgtct acacagccat 1350  
cgcagtgcag gagatacagg gaaacccggc ctcaccagcc caggactacc 1400  
gggcgctcta cgattataca gcgcagaacc cagatgagct ggacctgtcc 1450  
gcgggagaca tcctggaagg ggaggatggc tggaggactg tggagaggaa 1500  
cgggcagcgt ggcttcgtcc ctggttccta cctggagaag ctttgaggga 1550  
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Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu  
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Asp Gly Arg Lys Met Cys Lys Asp Met Glu Glu Leu Leu Arg Gln  
35 40 45  
Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile  
50 55 60  
Ala Arg Lys Ala Gly Gly Gln Thr Glu Ile Asn Ser Leu Arg Ala  
65 70 75  
Ser Phe Asp Ser Leu Lys Gln Gln Met Glu Asn Val Gly Ser Ser  
80 85 90  
His Ile Gln Leu Ala Leu Thr Leu Arg Glu Glu Leu Arg Ser Leu  
95 100 105  
Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Gly Met  
110 115 120  
Ala Val Pro Arg Gln Ser Asp Cys Met Glu Val Lys Ser Pro Ser  
125 130 135  
Trp Glu Tyr Glu Ala Val Met Asp Arg Val Gln Lys Ser Lys Leu



P1066P2.txt

| 140             | 145                 | 150                     |
|-----------------|---------------------|-------------------------|
| Ser Leu Tyr Lys | Lys Ala Met Glu Ser | Lys Lys Thr Tyr Glu Gln |
| 155             | 160                 | 165                     |
| Lys Cys Arg Asp | Ala Asp Asp Ala Glu | Gln Ala Phe Glu Arg Ile |
| 170             | 175                 | 180                     |
| Ser Ala Asn Gly | His Gln Lys Gln Val | Glu Lys Ser Gln Asn Lys |
| 185             | 190                 | 195                     |
| Ala Arg Gln Cys | Lys Asp Ser Ala Thr | Glu Ala Glu Arg Val Tyr |
| 200             | 205                 | 210                     |
| Arg Gln Ser Ile | Ala Gln Leu Glu Lys | Val Arg Ala Glu Trp Glu |
| 215             | 220                 | 225                     |
| Gln Glu His Arg | Thr Thr Cys Glu Ala | Phe Gln Leu Gln Glu Phe |
| 230             | 235                 | 240                     |
| Asp Arg Leu Thr | Ile Leu Arg Asn Ala | Leu Trp Val His Ser Asn |
| 245             | 250                 | 255                     |
| Gln Leu Ser Met | Gln Cys Val Lys Asp | Asp Glu Leu Tyr Glu Glu |
| 260             | 265                 | 270                     |
| Val Arg Leu Thr | Leu Glu Gly Cys Ser | Ile Asp Ala Asp Ile Asp |
| 275             | 280                 | 285                     |
| Ser Phe Ile Gln | Ala Lys Ser Thr Gly | Thr Glu Pro Pro Arg Phe |
| 290             | 295                 | 300                     |
| Ser Gly Leu Leu | His Gly Ser Pro Lys | Thr Thr Ser Ser Ala Ser |
| 305             | 310                 | 315                     |
| Ala Gly Ser Thr | Glu Thr Leu Thr Pro | Thr Pro Glu Arg Asn Glu |
| 320             | 325                 | 330                     |
| Gly Val Tyr Thr | Ala Ile Ala Val Gln | Glu Ile Gln Gly Asn Pro |
| 335             | 340                 | 345                     |
| Ala Ser Pro Ala | Gln Asp Tyr Arg Ala | Leu Tyr Asp Tyr Thr Ala |
| 350             | 355                 | 360                     |
| Gln Asn Pro Asp | Glu Leu Asp Leu Ser | Ala Gly Asp Ile Leu Glu |
| 365             | 370                 | 375                     |
| Gly Glu Asp Gly | Trp Trp Thr Val Glu | Arg Asn Gly Gln Arg Gly |
| 380             | 385                 | 390                     |
| Phe Val Pro Gly | Ser Tyr Leu Glu Lys | Leu                     |
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<210> 41
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<210> 42
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<212> DNA
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<210> 48

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<210> 53
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<210> 59

<211> 42

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<223> Synthetic oligonucleotide probe

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<210> 62

<211> 24

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<210> 63

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<223> Synthetic oligonucleotide probe

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<210> 66

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<400> 71  
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Pro Pro Ala Glu Trp Thr  
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Pro Pro Ser Glu Trp Thr  
 20



P1066P2.txt

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<211> 19

<212> PRT

<213> Artificial sequence

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1 5 10 15

Pro Ser Ala Trp